

GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: June 25, 2003, 14:38:41 ; Search time 25.6395 Seconds
(Without alignments)
843.812 Million cell updates/sec

Title: US-09-622-613b-6
Perfect score: 583
Sequence: 1 MDWLTFOKKHLTNTRDVC.....TFCVTCENQAPHFVGVGHC 105

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SPREMBL_21:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhbc:*
9: sp_organelle:*
10: sp_plant:*
11: sp_protist:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 578 | 99.1 | 127 | 13 | 0918V8 |
| 2 | 556 | 95.4 | 127 | 13 | 08UVX5 |
| 3 | 404.5 | 69.4 | 129 | 13 | 09DFY6 |
| 4 | 386 | 66.2 | 128 | 13 | 09DFY8 |
| 5 | 311 | 53.3 | 128 | 13 | 09DFY7 |
| 6 | 309 | 53.0 | 128 | 13 | 09DFY5 |
| 7 | 298 | 51.1 | 133 | 13 | 098SM0 |
| 8 | 292 | 50.1 | 133 | 13 | 09PMR7 |
| 9 | 286 | 49.1 | 133 | 13 | 098SL9 |
| 10 | 285 | 48.9 | 132 | 13 | 098SM2 |
| 11 | 282 | 48.4 | 133 | 13 | 098SL8 |
| 12 | 280 | 48.0 | 132 | 13 | 098SM1 |
| 13 | 275.5 | 47.3 | 132 | 13 | 09DF78 |
| 14 | 157.5 | 27.0 | 169 | 13 | 09W738 |
| 15 | 129 | 22.1 | 152 | 11 | 09JK15 |
| 16 | 127 | 21.8 | 157 | 11 | 09JK19 |

| | | | | | | |
|----|-------|------|-----|----|---------|---------------------|
| 17 | 126.5 | 21.7 | 153 | 11 | 09JK17 | 09jk17 mus saxicol |
| 18 | 126 | 21.6 | 157 | 11 | 09JKJ3 | 09jk13 meriones un |
| 19 | 125 | 21.4 | 157 | 11 | 09JKJ4 | 09jk14 meriones un |
| 20 | 123 | 21.1 | 154 | 11 | 09JKI8 | 09jk18 mus saxicol |
| 21 | 122 | 20.9 | 157 | 11 | 09JKJ1 | 09jk11 meriones un |
| 22 | 121 | 20.8 | 157 | 11 | 09JKJ2 | 09jk12 meriones un |
| 23 | 120.5 | 20.7 | 155 | 11 | 09JKH9 | 09jk19 mus pahari |
| 24 | 119.5 | 20.5 | 155 | 11 | 09JKI3 | 09jk13 mus saxicol |
| 25 | 116.5 | 20.0 | 155 | 11 | 09JKI6 | 09jk16 mus saxicol |
| 26 | 115.5 | 19.8 | 132 | 6 | 09TV25 | 09tv25 eullemur ful |
| 27 | 115.5 | 19.8 | 135 | 11 | 09JKI4 | 09jk14 mus saxicol |
| 28 | 115.5 | 19.8 | 155 | 11 | 09JKI2 | 09jk12 mus saxicol |
| 29 | 114.5 | 19.6 | 132 | 6 | 09TV24 | 09tv24 galago moho |
| 30 | 114.5 | 19.6 | 170 | 6 | 09BEC1 | 09bec1 tragulus ja |
| 31 | 113.5 | 19.5 | 119 | 6 | 09TSQ6 | 09tsq6 cercopithec |
| 32 | 113.5 | 19.5 | 119 | 6 | 09TV32 | 09tv32 gorilla gor |
| 33 | 113.5 | 19.5 | 155 | 11 | 09JKI34 | 09jk134 ratius norv |
| 34 | 113 | 19.4 | 156 | 11 | 09JKH7 | 09jk17 mus caroli |
| 35 | 113 | 19.4 | 156 | 11 | 09JKG6 | 09jk16 mus caroli |
| 36 | 112.5 | 19.3 | 119 | 6 | 09TV30 | 09tv30 saguinus oe |
| 37 | 112.5 | 19.3 | 155 | 11 | 09RI25 | 09ri25 mus musculu |
| 38 | 112.5 | 19.3 | 155 | 11 | 09JKH8 | 09jk18 mus pahari |
| 39 | 112 | 19.2 | 124 | 6 | 09TSE2 | 09tse2 bos taurus |
| 40 | 112 | 19.2 | 156 | 11 | 09JKG7 | 09jk17 mus caroli |
| 41 | 111.5 | 19.1 | 155 | 11 | 09JKG3 | 09jk13 mus caroli |
| 42 | 111 | 19.0 | 124 | 6 | 09SNE6 | 09sne6 bubalus bub |
| 43 | 111 | 19.0 | 156 | 6 | 08SQ04 | 08sq04 lemur calta |
| 44 | 111 | 19.0 | 156 | 11 | 09JKH5 | 09jk15 mus caroli |
| 45 | 111 | 19.0 | 156 | 11 | 09JKH4 | 09jk14 mus caroli |

ALIGNMENTS

RESULT 1

| | | | |
|-----------------------|--|------|------------|
| Q918V8 | PRELIMINARY: | PRT: | 127 AA. |
| AC | Q918V8: | | |
| DT | 01-OCT-2000 (TREMBLREL.15, Created) | | |
| DT | 01-OCT-2000 (TREMBLREL.15, Last sequence update) | | |
| DT | 01-DEC-2001 (TREMBLREL.19, Last annotation update) | | |
| DE | Onconase variant rap1L precursor. | | |
| OS | Rana pipiens (Northern leopard frog). | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| OC | Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana; | | |
| OX | NCBI_Taxid=8404; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RC | TISSUE=LIVER: | | |
| RX | MEDLINE=20330357; PubMed=10871370; | | |
| RT | Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.: | | |
| RT | "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a | | |
| RT | 3' UTR of unusual length and structure." | | |
| RL | Nucleic Acids Res. 28:2375-2382(2000). | | |
| DR | EMBL; AF165133; AACF76935.1; - | | |
| DR | HSSP; P22069; 10NC. | | |
| DR | InterPro: IPR001427; RNaseA. | | |
| DR | Pfam: PF00074; RNaseA; 1. | | |
| DR | ProDom: PD000535; RNaseA; 1. | | |
| DR | SMART: SM00092; RNase_Pc; 1. | | |
| DR | PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1. | | |
| KW | Signal. | | |
| FT | SIGNAL. 1 23 | | POTENTIAL. |
| SO | SEQUENCE 127 AA; 14491 MW; B8511DC5407AB69B CRC64; | | |
| Query Match | 99.1%; Score 578; DB 13; Length 127; | | |
| Best Local Similarity | 100.0%; Pred. No. 2e-58; | | |
| Matches | 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | |

OY 2 QDWLTFOKKHLTNTRDVCNNINSTNLFHCKDKKTFYFSRPEPKAKCKGIASKNVLT 61
Db 24 QDWLTFOKKHLTNTRDVCNNINSTNLFHCKDKKTFYFSRPEPKAKCKGIASKNVLT 83

| | | | |
|---|---|---|-----------------------------|
| RESULT | 5 | | |
| Q9DFY7 | PRELIMINARY: | PRT: | 128 AA. |
| ID | Q9DFY7 | | |
| AC | Q9DFY7; | | |
| DT | 01-MAR-2001 (TREMBLrel. 16, Created) | | |
| DT | 01-OCT-2001 (TREMBLrel. 18, Last sequence update) | | |
| DT | 01-DEC-2001 (TREMBLrel. 19, Last annotation update) | | |
| DE | RC-RNase3 ribonuclease precursor. | | |
| OS | Rana catesbeiana (Bull frog). | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| OC | Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana. | | |
| OX | NCBI_TaxID=8400; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RC | TISSUE=LIVER. | | |
| RX | MEDLINE=20512555; PubMed=11058105; | | |
| RA | Liao Y.-D., Huang H.C., Liew Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.; | | |
| RT | "Purification and cloning of cytotoxic ribonucleases from Rana | | |
| RT | catesbeiana (bullfrog)." | | |
| RL | Nucleic Acids Res. 28:4097-4104(2000). | | |
| DR | EMBL; AF242554; AACG1440.2; -. | | |
| DR | HSPB; P22069; IONC. | | |
| DR | InterPro: IPR001427; RNaseA. | | |
| DR | Pfam: PF00074; rnasea: 1. | | |
| DR | Prodrom: PD000535; RNaseA; 1. | | |
| DR | SMART: SM00092; RNase_Fc; 1. | | |
| DR | PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1. | | |
| KW | Signal. | | |
| FT | SIGNAL | 1 | 23 POTENTIAL. |
| FT | CHAIN | 24 | 128 RC-RNASE3 RIBONUCLEASE. |
| SO | SEQUENCE | 128 AA; 14517 MW; 2814986082E0587D CRC64; | |
| Query Match | | | |
| Best Local Similarity 53.3%; Score 311; DB 13; Length 128; | | | |
| Matches 57; Conservative 12; Mismatches 35; Indels 0; Gaps 0; | | | |
| Oy | 2 QDWTFORKHLTNRDVDCNNINMSTNLFHCDDKNTFIYSREPPYKAITGGIATANKVLT 61 | | |
| Dh | 24 QDWTEFORKHLLTDTRKKVCDEVMAKALFDCKRTNFIFIALGRVKALKCNIRDMTDLR 83 | | |
| Oy | 62 SEFLSDCNVTSRPCCKYLKLKSTNFCVTGCENAPVHPVGSHC 105 | | |
| Dh | 84 DAFLLPOCDRIKLPCCHYKLSSSTNTCLTCVNOLPIHFAGVSC 127 | | |
| RESULT 6 | | | |
| Q9DFY5 | PRELIMINARY: | PRT: | 128 AA. |
| ID | Q9DFY5 | | |
| AC | Q9DFY5; | | |
| DT | 01-MAR-2001 (TREMBLrel. 16, Created) | | |
| DT | 01-OCT-2001 (TREMBLrel. 18, Last sequence update) | | |
| DT | 01-DEC-2001 (TREMBLrel. 19, Last annotation update) | | |
| DE | RC-RNase6 ribonuclease precursor. | | |
| OS | Rana catesbeiana (Bull frog). | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| OC | Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana. | | |
| OX | NCBI_TaxID=8400; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RC | TISSUE=LIVER. | | |
| RX | MEDLINE=20512555; PubMed=11058105; | | |
| RA | Liao Y.-D., Huang H.C., Liew Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.; | | |
| RT | "Purification and cloning of cytotoxic ribonucleases from Rana | | |
| RT | catesbeiana (bullfrog)." | | |
| RL | Nucleic Acids Res. 28:4097-4104(2000). | | |
| RN | [2] | | |
| RP | SEQUENCE FROM N.A. | | |
| RC | TISSUE=LIVER. | | |
| RA | Liao Y.-D., Huang H.-C., Liew Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.; | | |
| RA | Submitted (Aug-2001) to the EMBL/GenBank/DDBJ databases. | | |
| DR | EMBL; AF242556; AAG31442.2; -. | | |
| DR | HSPB; P22069; IONC. | | |
| DR | InterPro: IPR001427; RNaseA. | | |

[illegible]

GN RCR.
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER.
 RX MEDLINE=98165825; PubMed=9497370;
 RA Huang H.C., Wang S.C., Liao Y.-D., Lu S.C., Liao Y.D.;
 RT "The Rana catesbeiana rcr gene encoding a cytotoxic ribonuclease.
 RT Tissue distribution, cloning, purification, cytotoxicity, and active
 RT residues for RNase activity.";
 RL J. Biol. Chem. 273:6395-6401(1998).
 DR EMBL: AF039104; AAD10702.1; -
 DR HSSP: P11916; IBC4.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA; 1.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase_Pc; 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
 KW Signal.
 FT SIGNAL.
 FT CHAIN 1 22 POTENTIAL.
 SQ SEQUENCE 133 AA; 14762 MW; A7D62594F7D16F0C CRC64;
 Query Match 50.1%; Score 292; DB 13; Length 133;
 Best Local Similarity 49.5%; Pred. No. 1e-25;
 Matches 55; Conservative 16; Mismatches 32; Indels 8; Gaps 3;

OY 2 QDWLTFOGKHILTNTRDVDCNNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIASKN 57
 Db 23 QWNAFEOGKHITNPISINCNTIMDNNTIYIGGCKKYNFTTISATTYKACIGG-VTNSN 81
 OY 58 VLTTSSEYLSDC---NVTSPCKYKLLKSTNFCVTCENQAPVHFGVGHIC 105
 Db 82 VLSPTRFQDLCTRIPTPCPYSSKRTETNYICVKNQDPVHFGAGIGRC 132

RESULT 9
 098SL9 ID PRELIMINARY; PRT; 133 AA.
 AC 098SL9;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE RNase A-type ribonuclease rc212 precursor.
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=21539506; PubMed=11683320;
 RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
 RT "Rapid diversification of RNase A superfamily ribonuclease from the
 RT bullfrog, Rana catesbeiana.";
 RL J. Mol. Evol. 53:31-38(2001).
 DR EMBL: AF351207; AAK30256.1; -
 DR HSSP: P11916; IBC4.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA; 1.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase_Pc; 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
 KW Signal.
 FT SIGNAL.
 FT CHAIN 1 22 POTENTIAL.
 SQ SEQUENCE 133 AA; 14615 MW; C878B236B26E54E CRC64;
 Query Match 49.1%; Score 286; DB 13; Length 133;
 Best Local Similarity 47.7%; Pred. No. 4.9e-25;
 Matches 53; Conservative 17; Mismatches 33; Indels 8; Gaps 3;

OY 2 QDWLTFOGKHILTNTRDVDCNNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIASKN 57
 Db 23 QWNAFEOGKHITNPISINCNTIMDNNTIYIGGCKKYNFTTISATTYKACIGG-VTNDK 81
 OY 58 VLTTSSEYLSDC---NVTSPCKYKLLKSTNFCVTCENQAPVHFGVGHIC 105
 Db 82 VLSPTRFQDLCTRIPTPCPYSSKRTETNYICVKNQDPVHFGAGIGRC 132

RESULT 10
 098SM2 ID PRELIMINARY; PRT; 132 AA.
 AC 098SM2;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE RNase A-type ribonuclease rc203 precursor (RC-RNase7 precursor).
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21539506; PubMed=11683320;
 RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
 RT "Rapid diversification of RNase A superfamily ribonuclease from the
 RT bullfrog, Rana catesbeiana.";
 RL J. Mol. Evol. 53:31-38(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER.
 RA Liao Y.-D., Tang P.-C., Jeng J.-T.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF351207; AAK30253.1; -
 DR EMBL: AF359578; AAL87036.1; -
 DR HSSP: P11916; IBC4.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA; 1.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase_Pc; 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
 KW Signal.
 FT SIGNAL.
 FT CHAIN 1 22 POTENTIAL.
 SQ SEQUENCE 132 AA; 14412 MW; 131A745187978687 CRC64;

Query Match 48.9%; Score 285; DB 13; Length 132;
 Best Local Similarity 47.7%; Pred. No. 6.3e-25;
 Matches 53; Conservative 14; Mismatches 36; Indels 8; Gaps 3;

OY 2 QDWLTFOGKHILTNTRDVDCNNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIASKN 57
 Db 23 QWNAFEOGKHITNPISINCNTIMDNNTIYIGGCKKYNFTTISATTYKACIGG-VTNSN 81
 OY 58 VLTTSSEYLSDC---NVTSPCKYKLLKSTNFCVTCENQAPVHFGVGHIC 105
 Db 82 VLSPTRFQDLCTRIPTPCPYSSKRTETNYICVKNQDPVHFGAGIGRC 132

RESULT 11
 098SL8 ID PRELIMINARY; PRT; 133 AA.
 AC 098SL8;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE RNase A-type ribonuclease rc218 precursor.
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE FROM N.A.

